SEQUENCE LISTING

<110> Abbott Laboratories
      Mukerji, Pradip
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      Pereira, Suzette L.

<120> DESATURASE GENES, ENZYMES ENCODED
   THEREBY, AND USES THEREOF

<130> 6884.US.01

<140> 10/060,793
<141> 2002-01-30

<160> 60

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1144

<400> 1
atccgcgccg ccatccccaa gcactgctgg gtcaag   36

<210> 2
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1119

<221> misc_feature
<222> (21)...(21)
<223> y = t/u or c at position 21

<221> misc_feature
<222> (33)...(33)
<223> y = t/u or c at position 33

<400> 2
gccctcttcg tcctcggcca ygactgcggc cayggctcgt tctcg   45

<210> 3
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1118

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<221> misc_feature
<222> (4)...(4)
<223> r = g or a at position 4

<221> misc_feature
<222> (10)...(10)
<223> r = g or a at position 10

<221> misc_feature
<222> (30)...(31)
<223> r = g or a at positions 30-31

<221> misc_feature
<222> (34)...(34)
<223> r = g or a at position 34

<221> misc_feature
<222> (38)...(38)
<223> r = g or a at poisition 38

<221> misc_feature
<222> (39)...(39)
<223> y = t/u or c at position 39

<221> misc_feature
<222> (43)...(43)
<223> r = g or a at position 43

<400> 3
gagrtggtar tgggggatct gggggaagar rtgrtggryg acrtg                          45

<210> 4
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1121

<221> misc_feature
<222> (9)...(9)
<223> y = t/u or c at position 9

<221> misc_feature
<222> (27)...(27)
<223> y = t/u or c at position 27

<221> misc_feature
<222> (36)...(36)
<223> y = t/u or c at position 36

<221> misc_feature
<222> (39)...(39)
<223> y = t/u or c at position 39

<400> 4
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ccctaccayg gctggcgcat ctcgcaycgc acccaycayc agaac   45

<210> 5
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1122

<221> misc_feature
<222> (7)...(7)
<223> r = g or a at position 7

<221> misc_feature
<222> (10)...(10)
<223> r = g or a at position 10

<221> misc_feature
<222> (37)...(37)
<223> r = g or a at position 37

<400> 5
gttctgrtgr tgggtccgrt gcgagatgcg ccagccrtgg taggg   45

<210> 6
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1146

<221> misc_feature
<222> (13)...(13)
<223> s = g or c at position 13

<221> misc_feature
<222> (19)...(19)
<223> k = g or t/u at position 19

<400> 6
ggctcgcact tcsaccccka ctcggacctc ttcgtc   36

<210> 7
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1147

<221> misc_feature
<222> (18)...(18)
<223> m = a or c at position 18

<221> misc_feature

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<222> (24)...(24)
<223> w = a or t/u at position 24

<400> 7
gacgaagagg tccgagtmgg ggtwgaagtg cgagcc                              36

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1148

<221> misc_feature
<222> (9)...(9)
<223> k = g or t/u at position 9

<221> misc_feature
<222> (30)...(30)
<223> w = a or t/u at position 30

<221> misc_feature
<222> (32)...(32)
<223> s = g or c at position 32

<400> 8
gcgctggakg gtggtgaggc cgccgcggaw gsacgacca                           39

<210> 9
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1114

<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

<221> misc_feature
<222> (16)...(16)
<223> r = g or a at position 16

<221> misc_feature
<222> (25)...(25)
<223> r = g or a at position 25

<221> misc_feature
<222> (40)...(40)
<223> r = g or a at position 40

<221> misc_feature
<222> (43)...(43)
<223> r = g or a at position 43
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<400> 9
ctgggggaag agrtgrtgga tgacrtgggt gccgatgtcr tgrtg                45
```

```
<210> 10
<211> 45
<212> DNA
<213> Artificial Sequence
```

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<220>
<223> Reverse Primer RO1116
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<221> misc_feature
<222> (12)...(12)
<223> y = t/u or c at position 12
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```
<221> misc_feature
<222> (16)...(16)
<223> r = g or a at position 16
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<221> misc_feature
<222> (22)...(22)
<223> r = g or a at position 22
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<221> misc_feature
<222> (33)...(33)
<223> k = g or t/u at position 33
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<221> misc_feature
<222> (42)...(43)
<223> r = g or at at positions 42-43
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<400> 10
ggtggcctcg aygagrtggt artgggggat ctkggggaag arrtg                45
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<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence
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<220>
<223> Reverse Primer RO1118
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<221> misc_feature
<222> (4)...(4)
<223> r = g or a at position 4
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```
<221> misc_feature
<222> (10)...(10)
<223> r = g or a at position 10
```

```
<221> misc_feature
<222> (30)...(31)
<223> r = g or a at positions 30-31
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<221> misc_feature
<222> (34)...(34)
<223> r = g or a at position 34
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<221> misc_feature
<222> (38)...(38)
<223> r = g or a at position 38

<221> misc_feature
<222> (39)...(39)
<223> y = t/u or c at position 39

<221> misc_feature
<222> (43)...(43)
<223> r = g or a at position 43

<400> 11
gagrtggtar tggggatct ggggaagar rtgrtggryg acrtg   45

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1188

<400> 12
tacgcgtacc tcacgtactc gctcg   25

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1189

<400> 13
ttcttgcacc acaacgacga agcgacg   27

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1190

<400> 14
ggagtggacg tacgtcaagg gcaac   25

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1191

<400> 15
tcaagggcaa cctctcgagc gtcgac   26

<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO898

<400> 16
cccagtcacg acgttgtaaa acgacggcca g   31

<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO899

<400> 17
agcggataac aatttcacac aggaaacagc   30

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1185

<400> 18
ggtaaaagat ctcgtccttg tcgatgttgc   30

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1186

<400> 19
gtcaaagtgg ctcatcgtgc   20

<210> 20
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1187

<400> 20
cgagcgagta cgtgaggtac gcgtac   26

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<210> 21
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1212

<400> 21
tcaacagaat tcatgaccga ggataagacg aaggtcgagt tcccg                    45

<210> 22
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1213

<400> 22
aaaagaaagc ttcgcttcct agtcttagtc cgacttggcc ttggc                    45

<210> 23
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1221

<400> 23
tcaacaaagc ttatgaccga ggataagacg aaggtcgagt tcccg                    45

<210> 24
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1222

<400> 24
aaaagagaat tccgcttcct agtcttagtc cgacttggcc ttggc                    45

<210> 25
<211> 1077
<212> DNA
<213> Saprolegnia diclina

<400> 25
atgactgagg ataagacgaa ggtcgagttc ccgacgctca cggagctcaa gcactcgatc    60
ccgaacgcgt gctttgagtc gaacctcggc ctctcgctct actacacggc ccgcgcgatc   120
ttcaacgcgt cggcctcggc ggcgctgctc tacgcggcgc gctcgacgcc gttcattgcc   180
gataacgttc tgctccacgc gctcgtttgc gccacctaca tctacgtgca gggcgtcatc   240
ttctggggct tcttcacggt cggccacgac tgcggccact cggccttctc gcgctaccac   300
agcgtcaact ttatcatcgg ctgcatcatg cactctgcga ttttgacgcc gttcgagagc   360
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```
tggcgcgtga cgcaccgcca ccaccacaag aacacgggca acattgataa ggacgagatc      420
ttttacccgc accggtcggt caaggacctc caggacgtgc gccaatgggt ctacacgctc      480
ggcggtgcgt ggtttgtcta cttgaaggtc gggtatgccc cgcgcacgat gagccacttt      540
gacccgtggg acccgctcct ccttcgccgc gcgtcggccg tcatcgtgtc gctcggcgtc      600
tgggccgcct tcttcgccgc gtacgcgtac ctcacatact cgctcggctt tgccgtcatg      660
ggcctctact actatcgcgc gctctttgtc tttgcttcgt tcctcgtcat tacgaccttc      720
ttgcaccaca acgacgaagc gacgccgtgg tacggcgact cggagtggac gtacgtcaag      780
ggcaacctct cgagcgtcga ccgctcgtac ggcgcgttcg tggacaacct gagccaccac      840
attggcacgc accaggtcca ccacttgttc ccgatcattc cgcactacaa gctcaacgaa      900
gccaccaagc actttgcggc cgcgtacccg cacctcgtga gcaggaacga cgagcccatc      960
atcacggcct tcttcaagac cgcgcgcacctc tttgtcaact acggcgctgt gcccgagacg     1020
gcgcagatct tcacgctcaa agagtcggcc gcggccgcca aggccaagtc ggactaa         1077
```

<210> 26
<211> 358
<212> PRT
<213> Saprolegnia diclina

<400> 26

```
Met Thr Glu Asp Lys Thr Lys Val Glu Phe Pro Thr Leu Thr Glu Leu
1               5                   10                  15
Lys His Ser Ile Pro Asn Ala Cys Phe Glu Ser Asn Leu Gly Leu Ser
            20                  25                  30
Leu Tyr Tyr Thr Ala Arg Ala Ile Phe Asn Ala Ser Ala Ser Ala Ala
        35                  40                  45
Leu Leu Tyr Ala Ala Arg Ser Thr Pro Phe Ile Ala Asp Asn Val Leu
    50                  55                  60
Leu His Ala Leu Val Cys Ala Thr Tyr Ile Tyr Val Gln Gly Val Ile
65                  70                  75                  80
Phe Trp Gly Phe Phe Thr Val Gly His Asp Cys Gly His Ser Ala Phe
                85                  90                  95
Ser Arg Tyr His Ser Val Asn Phe Ile Ile Gly Cys Ile Met His Ser
            100                 105                 110
Ala Ile Leu Thr Pro Phe Glu Ser Trp Arg Val Thr His Arg His His
        115                 120                 125
His Lys Asn Thr Gly Asn Ile Asp Lys Asp Glu Ile Phe Tyr Pro His
    130                 135                 140
Arg Ser Val Lys Asp Leu Gln Asp Val Arg Gln Trp Val Tyr Thr Leu
145                 150                 155                 160
Gly Gly Ala Trp Phe Val Tyr Leu Lys Val Gly Tyr Ala Pro Arg Thr
                165                 170                 175
Met Ser His Phe Asp Pro Trp Asp Pro Leu Leu Leu Arg Arg Ala Ser
            180                 185                 190
Ala Val Ile Val Ser Leu Gly Val Trp Ala Ala Phe Phe Ala Ala Tyr
        195                 200                 205
Ala Tyr Leu Thr Tyr Ser Leu Gly Phe Ala Val Met Gly Leu Tyr Tyr
    210                 215                 220
Tyr Ala Pro Leu Phe Val Phe Ala Ser Phe Leu Val Ile Thr Thr Phe
225                 230                 235                 240
Leu His His Asn Asp Glu Ala Thr Pro Trp Tyr Gly Asp Ser Glu Trp
                245                 250                 255
Thr Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala
            260                 265                 270
Phe Val Asp Asn Leu Ser His His Ile Gly Thr His Gln Val His His
        275                 280                 285
Leu Phe Pro Ile Ile Pro His Tyr Lys Leu Asn Glu Ala Thr Lys His
    290                 295                 300
```

```
Phe Ala Ala Ala Tyr Pro His Leu Val Arg Arg Asn Asp Glu Pro Ile
305                 310                 315                 320
Ile Thr Ala Phe Phe Lys Thr Ala His Leu Phe Val Asn Tyr Gly Ala
                325                 330                 335
Val Pro Glu Thr Ala Gln Ile Phe Thr Leu Lys Glu Ser Ala Ala Ala
            340                 345                 350
Ala Lys Ala Lys Ser Asp
            355
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```
<210> 27
<211> 1413
<212> DNA
<213> Saprolegnia diclina

<400> 27
atggccccgc agacggagct ccgccagcgc cacgccgccg tcgccgagac gccggtggcc    60
ggcaagaagg cctttacatg gcaggaggtc gcgcagcaca acacggcggc ctcggcctgg   120
atcattatcc gcggcaaggt ctacgacgtg accgagtggg ccaacaagca ccccggcggc   180
cgcgagatgg tgctgctgca cgccggtcgc gaggccaccg acacgttcga ctcgtaccac   240
ccgttcagcg acaaggccga gtcgatcttg aacaagtatg agattggcac gttcacgggc   300
ccgtccgagt ttcgaccttt caagccggac acgggcttct acaaggagtg ccgcaagcgc   360
gttggcgagt acttcaagaa gaacaacctc catccgcagg acggcttccc gggcctctgg   420
cgcatgatgg tcgtgtttgc ggtcgccggc ctcgccttgt acggcatgca cttttcgact   480
atctttgcgc tgcagctcgc ggccgcggcg ctctttggcg tctgccaggc gctgccgctg   540
ctccacgtca tgcacgactc gtcgcacgcg tcgtacacca acatgccgtt cttccattac   600
gtcgtcggcc gctttgccat ggactggttt gccggcggct cgatggtgtc atggctcaac   660
cagcacgtcg tgggccacca catctcacacg aacgtcgcgg gctcggaccc ggatcttccg   720
gtcaacatgg acggcgacat ccgccgcatc gtgaaccgcc aggtgttcca gcccatgtac   780
gcattccagc acatctacct tccgccgctc tatggcgtgc ttggcctcaa gttccgcatc   840
caggacttca ccgacacgtt cggctcgcac acgaacggcc cgatccgcgt caacccgcac   900
gcgctctcga cgtggatggc catgatcagc tccaagtcgt tctgggcctt ctaccgcgtg   960
taccttccgc ttgccgtgct ccagatgccc atcaagacgt accttgcgat cttcttcctc  1020
gccgagtttg tcacgggctg gtacctcgcg ttcaacttcc aagtaagcca tgtctcgacc  1080
gagtgcggct acccatgcgg cgacgaggcc aagatggcgc tccaggacga gtgggcagtc  1140
tcgcaggtca agacgtcggt cgactacgcc catgctcgt ggatgacgac gttccttgcc  1200
ggcgcgctca actaccaggt cgtgcaccac ttgttcccca gcgtgtcgca gtaccactac  1260
ccggcgatcg cgcccatcat cgtcgacgtc tgcaaggagt acaacatcaa gtacgccatc  1320
ttgccggact ttacggcggc gttcgttgcc cacttgaagc acctccgcaa catgggccag  1380
cagggcatcg ccgccacgat ccacatgggc taa                                1413
```

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<210> 28
<211> 819
<212> DNA
<213> Thraustochytrid sp.

<400> 28
atggcaaaca gcagcgtgtg ggatgatgtg gtgggccgcg tggagaccgg cgtggaccag    60
tggatggatg gcgccaagcc gtacgcactc accgatgagt cccgatgat ggacgtgtcc   120
accatgctgg cattcgaggt gggatacatg gccatgctgc tcttcggcat cccgatcatg   180
aagcagatgg agaagccttt tgagctcaag accatcaagc tcttgcacaa cttgtttctc   240
ttcggacttt ccttgtacat gtgcgtggag accatccgcc aggctatcct cggaggctac   300
aaagtgtttg gaaacgacat ggagaagggc aacgagtctc atgctcaggg catgtctcgc   360
atcgtgtacg tgttctgcgt gtccaaggca tacgagttct tggatacgc catcatgatc   420
ctttgcaaga agttcaacca ggtttccttc ttgcatgtgt accaccatgc caccatttt   480
gccatctggt gggctatcgc caagtacgct ccaggaggtg atgcgtactt ttcagtgatc   540
ctcaactctt tcgtcgcacac cgtcatgtac gcatactact tcttctcctc ccaagggttc   600
gggttcgtga agccaatcaa gccgtacatc accaccctc agatgaccca gttcatggca   660
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```
atgcttgtgc agtccttgta cgactacctc ttcccatgcg actacccaca ggctcttgtg    720
cagcttcttg gagtgtacat gatcaccttg cttgccctct tcggcaactt ttttgtgcag    780
agctatctta aaaagccaaa aaagagcaag accaactaa                           819
```

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<210> 29
<211> 515
<212> PRT
<213> Saprolegnia diclina

<400> 29
Met Thr Val Gly Phe Asp Glu Thr Val Thr Met Asp Thr Val Arg Asn
1               5                   10                  15
His Asn Met Pro Asp Asp Ala Trp Cys Ala Ile His Gly Thr Val Tyr
            20                  25                  30
Asp Ile Thr Lys Phe Ser Lys Val His Pro Gly Gly Asp Ile Ile Met
        35                  40                  45
Leu Ala Ala Gly Lys Glu Ala Thr Ile Leu Phe Glu Thr Tyr His Ile
    50                  55                  60
Lys Gly Val Pro Asp Ala Val Leu Arg Lys Tyr Lys Val Gly Lys Leu
65                  70                  75                  80
Pro Gln Gly Lys Lys Gly Glu Thr Thr Ser His Met Pro Thr Gly Leu Asp
            85                  90                  95
Ser Ala Ser Tyr Tyr Ser Trp Asp Ser Glu Phe Tyr Arg Val Leu Arg
        100                 105                 110
Glu Arg Val Ala Lys Lys Leu Ala Glu Pro Gly Leu Met Gln Arg Ala
    115                 120                 125
Arg Met Glu Leu Trp Ala Lys Ala Ile Phe Leu Leu Ala Gly Phe Trp
130                 135                 140
Gly Ser Leu Tyr Ala Met Cys Val Leu Asp Pro His Gly Gly Ala Met
145                 150                 155                 160
Val Ala Ala Val Thr Leu Gly Val Phe Ala Ala Phe Val Gly Thr Cys
            165                 170                 175
Ile Gln His Asp Gly Ser His Gly Ala Phe Ser Lys Ser Arg Phe Met
        180                 185                 190
Asn Lys Ala Ala Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Met
    195                 200                 205
Thr Trp Glu Met Gln His Val Leu Gly His His Pro Tyr Thr Asn Leu
    210                 215                 220
Ile Glu Met Glu Asn Gly Leu Ala Lys Val Lys Gly Ala Asp Val Asp
225                 230                 235                 240
Pro Lys Lys Val Asp Gln Glu Ser Asp Pro Asp Val Phe Ser Thr Tyr
            245                 250                 255
Pro Met Leu Arg Leu His Pro Trp His Arg Gln Arg Phe Tyr His Lys
        260                 265                 270
Phe Gln His Leu Tyr Ala Pro Leu Ile Phe Gly Phe Met Thr Ile Asn
    275                 280                 285
Lys Val Ile Ser Gln Asp Val Gly Val Val Leu Arg Lys Arg Leu Phe
290                 295                 300
Gln Ile Asp Ala Asn Cys Arg Tyr Gly Ser Pro Trp Asn Val Ala Arg
305                 310                 315                 320
Phe Trp Ile Met Lys Leu Leu Thr Thr Leu Tyr Met Val Ala Leu Pro
            325                 330                 335
Met Tyr Met Gln Gly Pro Ala Gln Gly Leu Lys Leu Phe Phe Met Ala
        340                 345                 350
His Phe Thr Cys Gly Glu Val Leu Ala Thr Met Phe Ile Val Asn His
    355                 360                 365
Ile Ile Glu Gly Val Ser Tyr Ala Ser Lys Asp Ala Val Lys Gly Val
```

```
     370                        375                        380
Met Ala Pro Pro Arg Thr Val His Gly Val Thr Pro Met Gln Val Thr
385                        390                        395                        400
Gln Lys Ala Leu Ser Ala Ala Glu Ser Thr Lys Ser Asp Ala Asp Lys
                    405                        410                        415
Thr Thr Met Ile Pro Leu Asn Asp Trp Ala Ala Val Gln Cys Gln Thr
               420                        425                        430
Ser Val Asn Trp Ala Val Gly Ser Trp Phe Trp Asn His Phe Ser Gly
          435                        440                        445
Gly Leu Asn His Gln Ile Glu His His Cys Phe Pro Gln Asn Pro His
     450                        455                        460
Thr Val Asn Val Tyr Ile Ser Gly Ile Val Lys Glu Thr Cys Glu Glu
465                        470                        475                        480
Tyr Gly Val Pro Tyr Gln Ala Glu Ile Ser Leu Phe Ser Ala Tyr Phe
               485                        490                        495
Lys Met Leu Ser His Leu Arg Thr Leu Gly Asn Glu Asp Leu Thr Ala
          500                        505                        510
Trp Ser Thr
     515
```

<210> 30
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO967

<221> misc_feature
<222> (4)...(4)
<223> s = g or c at position 4

<221> misc_feature
<222> (12)...(12)
<223> s = g or c at position 12

<221> misc_feature
<222> (30)...(30)
<223> s = g or c at position 30

<221> misc_feature
<222> (31)...(31)
<223> k = g or t/u at position 31

<221> misc_feature
<222> (32)...(32)
<223> s = g or c at position 32

<400> 30
ccgsagttca csatcaagga gatccgcgas kscatcccgg cccactgctt c   51

<210> 31
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Reverse Primer RO968

<221> misc_feature
<222> (2)...(2)
<223> r = g or a at position 2

<221> misc_feature
<222> (3)...(3)
<223> s = g or c at position 3

<221> misc_feature
<222> (12)...(12)
<223> k = g or t/u at position 12

<221> misc_feature
<222> (17)...(17)
<223> w = a or t/u at position 17

<221> misc_feature
<222> (18)...(18)
<223> m = a or c at position 18

<221> misc_feature
<222> (19)...(19)
<223> s = g or c at position 19

<221> misc_feature
<222> (41)...(41)
<223> w = a or t/u at position 41

<221> misc_feature
<222> (42)...(42)
<223> r = g or a at position 42

<400> 31
grscttcttg akgtggwmsg tggcctcctc ggcgtggtag wrcggcat   48

<210> 32
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO964

<221> misc_feature
<222> (3)...(4)
<223> s = g or c at positions 3-4

<221> misc_feature
<222> (25)...(25)
<223> r = g or a at position 25

<221> misc_feature
<222> (36)...(36)
<223> s = g or c at position 36

<400> 32
ccsstctact gggcctgcca gggtrtcgtc ctcacsggtg tctgg   45

<210> 33
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO965

<221> misc_feature
<222> (3)...(4)
<223> s = g or c at positions 3-4

<221> misc_feature
<222> (16)...(16)
<223> r = g or a at position 16

<221> misc_feature
<222> (17)...(17)
<223> y = t/u or c at position 17

<221> misc_feature
<222> (18)...(18)
<223> s = g or c at position 18

<221> misc_feature
<222> (25)...(25)
<223> r = g or a at position 25

<221> misc_feature
<222> (31)...(31)
<223> k = g or t/u at position 31

<221> misc_feature
<222> (33)...(33)
<223> y = t/u or c at position 33

<221> misc_feature
<222> (36)...(36)
<223> s = g or c at position 36

<400> 33
ccsstctact ggatcrysca gggtrtcgtc kgyacsggtg tctgg   45

<210> 34
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO966

<221> misc_feature
<222> (19)...(19)
<223> s = g or c at position 19

```
<221> misc_feature
<222> (20)...(21)
<223> m = a or c at positions 20-21

<221> misc_feature
<222> (30)...(30)
<223> r = g or a at position 30

<400> 34
ggcgtggtag tgcggcatsm mcgagaagar gtggtgggcg acgtg                45

<210> 35
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO975

<400> 35
cacgtacctc cagcacacgg acacctacg                                  29

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO976

<400> 36
gatcgacagc gcgatccacc acattgc                                    27

<210> 37
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO977

<400> 37
caaatggtaa aagctagtgg cagcgctgc                                  29

<210> 38
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO978

<400> 38
agtacgtgcc ctggacgaac cagtagatg                                  29

<210> 39
```

```
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1051

<400> 39
tcaacagaat tcatgtgcaa aggtcaagct ccttccaagg ccgacgtg                    48

<210> 40
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1057

<400> 40
aaaagaaagc ttttacttttt cctcgagctt gcgcttgtaa aacacaac                  48

<210> 41
<211> 1182
<212> DNA
<213> Saprolegnia diclina

<400> 41
atgtgcaaag gtcaagctcc ttccaaggcc gacgtgttcc acgctgcggg gtaccgcccg      60
gtcgccggca cgcccgagcc gctgccgctg gagccccga cgatcacgct caaggacctg      120
cgcgcggcga tcccggccca ctgctttgag cgcagcgctg ccactagctt ttaccatttg      180
gccaagaacc ttgcgatctg cgccggccgtg ttcgccgttg gcctcaagct cgcggctgcc     240
gacttgcccg tcgcggccaa gctggtcgcg tggcccatct actggttcgt ccagggcacg      300
tactttacgg gcatctgggt cattgcgcac gaatgcggcc accaggcgtt ctcggcgtcc     360
gagatcctca acgacacggt cggtatcatt cttcactcgc tcctctttgt gccgtaccac      420
agctggaaga tcacgcaccg ccgccaccac tccaacacgg gcagctgcga gaacgacgag      480
gtgtttacgc cgacgccgcg gtccgtcgtc gaggccaagc acgaccactc gctcctcgaa      540
gagagcccgc tctacaacct gtacggcatc gtcatgatgc ttctcgtggg ctggatgccg      600
ggctacctct tcttcaacgc gaccggcccg accaagtacg ctggcctcgc caagtcgcac      660
ttcaacccgt acgcagcctt tttcctccca aaggagcgcc tcagcatctg gtggagcgac      720
ctctgcttcc tcgcggcctt gtacggcttt ggctacggcg tctcggtctt cggcctcctc     780
gatgtcgccc gccactacat cgtgccgtac ctcatttgca acgcgtacct cgtgctcatc      840
acgtacctcc agcacacgga tacgtacgtg ccccacttcc gcggcgacga gtggaactgg      900
ctgcgcggcg cgctctgcac cgtcgacgcc tcgttcggcg cgtggatcga cagcgcgatc      960
caccacattg ccgacacgca cgtgacgcac cacatttttct ccaagacgcc cttctaccac     1020
gcgatcgagg cgaccgacgc catcacgccc ctcctcggca agtactacct catcgacccg     1080
acgccgatcc cgctggccgct ctggcgctcg ttcacgcact gcaagtacgt cgaggacgac     1140
ggcaacgttg tgttttacaa gcgcaagctc gaggaaaagt aa                        1182

<210> 42
<211> 393
<212> PRT
<213> Saprolegnia diclina

<400> 42
Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala
1               5                   10                  15
Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Leu Glu Pro
```

```
          20                   25                   30
Pro Thr Ile Thr Leu Lys Asp Leu Arg Ala Ala Ile Pro Ala His Cys
         35                   40                   45
Phe Glu Arg Ser Ala Ala Thr Ser Phe Tyr His Leu Ala Lys Asn Leu
    50                   55                   60
Ala Ile Cys Ala Gly Val Phe Ala Val Gly Leu Lys Leu Ala Ala Ala
65                   70                   75                   80
Asp Leu Pro Leu Ala Ala Lys Leu Val Ala Trp Pro Ile Tyr Trp Phe
              85                   90                   95
Val Gln Gly Thr Tyr Phe Thr Gly Ile Trp Val Ile Ala His Glu Cys
         100                  105                  110
Gly His Gln Ala Phe Ser Ala Ser Glu Ile Leu Asn Asp Thr Val Gly
         115                  120                  125
Ile Ile Leu His Ser Leu Leu Phe Val Pro Tyr His Ser Trp Lys Ile
    130                  135                  140
Thr His Arg Arg His His Ser Asn Thr Gly Ser Cys Glu Asn Asp Glu
145                  150                  155                  160
Val Phe Thr Pro Thr Pro Arg Ser Val Val Glu Ala Lys His Asp His
              165                  170                  175
Ser Leu Leu Glu Glu Ser Pro Leu Tyr Asn Leu Tyr Gly Ile Val Met
         180                  185                  190
Met Leu Leu Val Gly Trp Met Pro Gly Tyr Leu Phe Phe Asn Ala Thr
    195                  200                  205
Gly Pro Thr Lys Tyr Ala Gly Leu Ala Lys Ser His Phe Asn Pro Tyr
    210                  215                  220
Ala Ala Phe Phe Leu Pro Lys Glu Arg Leu Ser Ile Trp Trp Ser Asp
225                  230                  235                  240
Leu Cys Phe Leu Ala Ala Leu Tyr Gly Phe Gly Tyr Gly Val Ser Val
              245                  250                  255
Phe Gly Leu Leu Asp Val Ala Arg His Tyr Ile Val Pro Tyr Leu Ile
         260                  265                  270
Cys Asn Ala Tyr Leu Val Leu Ile Thr Tyr Leu Gln His Thr Asp Thr
    275                  280                  285
Tyr Val Pro His Phe Arg Gly Asp Glu Trp Asn Trp Leu Arg Gly Ala
    290                  295                  300
Leu Cys Thr Val Asp Arg Ser Phe Gly Ala Trp Ile Asp Ser Ala Ile
305                  310                  315                  320
His His Ile Ala Asp Thr His Val Thr His His Ile Phe Ser Lys Thr
              325                  330                  335
Pro Phe Tyr His Ala Ile Glu Ala Thr Asp Ala Ile Thr Pro Leu Leu
         340                  345                  350
Gly Lys Tyr Tyr Leu Ile Asp Pro Thr Pro Ile Pro Leu Ala Leu Trp
         355                  360                  365
Arg Ser Phe Thr His Cys Lys Tyr Val Glu Asp Asp Gly Asn Val Val
    370                  375                  380
Phe Tyr Lys Arg Lys Leu Glu Glu Lys
385                  390
```

```
<210> 43
<211> 393
<212> PRT
<213> Saprolegnia diclina

<400> 43
Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala
1               5                   10                  15
Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Leu Glu Pro
```

```
            20                    25                    30
Pro Thr Ile Thr Leu Lys Asp Leu Arg Ala Ala Ile Pro Ala His Cys
        35                    40                    45
Phe Glu Arg Ser Ala Ala Thr Ser Phe Tyr His Leu Ala Lys Asn Leu
    50                    55                    60
Ala Ile Cys Ala Gly Val Phe Ala Val Gly Leu Lys Leu Ala Ala Ala
65                    70                    75                    80
Asp Leu Pro Leu Ala Ala Lys Leu Val Ala Trp Pro Ile Tyr Trp Phe
                85                    90                    95
Val Gln Gly Thr Tyr Phe Thr Gly Ile Trp Val Ile Ala His Glu Cys
            100                   105                   110
Gly His Gln Ala Phe Ser Ala Ser Glu Ile Leu Asn Asp Thr Val Gly
        115                   120                   125
Ile Ile Leu His Ser Leu Leu Phe Val Pro Tyr His Ser Trp Lys Ile
    130                   135                   140
Thr His Arg Arg His His Ser Asn Thr Gly Ser Cys Glu Asn Asp Glu
145                   150                   155                   160
Val Phe Thr Pro Thr Pro Arg Ser Val Val Glu Ala Lys His Asp His
                165                   170                   175
Ser Leu Leu Glu Glu Ser Pro Leu Tyr Asn Leu Tyr Gly Ile Val Met
            180                   185                   190
Met Leu Leu Val Gly Trp Met Pro Gly Tyr Leu Phe Phe Asn Ala Thr
        195                   200                   205
Gly Pro Thr Lys Tyr Ala Gly Leu Ala Lys Ser His Phe Asn Pro Tyr
    210                   215                   220
Ala Ala Phe Phe Leu Pro Lys Glu Arg Leu Ser Ile Trp Trp Ser Asp
225                   230                   235                   240
Leu Cys Phe Leu Ala Ala Leu Tyr Gly Phe Gly Tyr Gly Val Ser Val
                245                   250                   255
Phe Gly Leu Leu Asp Val Ala Arg His Tyr Ile Val Pro Tyr Leu Ile
            260                   265                   270
Cys Asn Ala Tyr Leu Val Leu Ile Thr Tyr Leu Gln Gln His Thr Asp Thr
        275                   280                   285
Tyr Val Pro His Phe Arg Gly Asp Glu Trp Asn Trp Leu Arg Gly Ala
    290                   295                   300
Leu Cys Thr Val Asp Arg Ser Phe Gly Ala Trp Ile Asp Ser Ala Ile
305                   310                   315                   320
His His Ile Ala Asp Thr His Val Thr His His Ile Phe Ser Lys Thr
                325                   330                   335
Pro Phe Tyr His Ala Ile Glu Ala Thr Asp Ala Ile Thr Pro Leu Leu
            340                   345                   350
Gly Lys Tyr Tyr Leu Ile Asp Pro Thr Pro Ile Pro Leu Ala Leu Trp
        355                   360                   365
Arg Ser Phe Thr His Cys Lys Tyr Val Glu Asp Asp Gly Asn Val Val
    370                   375                   380
Phe Tyr Lys Arg Lys Leu Glu Glu Lys
385                   390
```

```
<210> 44
<211> 359
<212> PRT
<213> Synechocystis sp.

<220>
<221> VARIANT
<222> (315)...(315)
<223> Xaa = Unknown or Other at position 315
```

```
<221> VARIANT
<222> (331)...(331)
<223> Xaa = Unknown or Other at position 331

<400> 44
Tyr Phe Phe Leu Asp Val Gly Leu Ile Ala Gly Phe Tyr Ala Leu Ala
1               5                   10                  15
Ala Tyr Leu Asp Ser Trp Phe Phe Tyr Pro Ile Phe Trp Leu Ile Gln
        20                  25                  30
Gly Thr Leu Phe Trp Ser Leu Phe Val Val Gly His Asp Cys Gly His
    35                  40                  45
Gly Ser Phe Ser Lys Ser Lys Thr Leu Asn Asn Trp Ile Gly His Leu
50                  55                  60
Ser His Thr Pro Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His
65                  70                  75                  80
Arg Thr His His Ala Asn Thr Gly Asn Ile Asp Thr Asp Glu Ser Trp
            85                  90                  95
Tyr Pro Val Ser Glu Gln Lys Tyr Asn Gln Met Ala Trp Tyr Glu Lys
        100                 105                 110
Leu Leu Arg Phe Tyr Leu Pro Leu Ile Ala Tyr Pro Ile Tyr Leu Phe
        115                 120                 125
Arg Arg Ser Pro Asn Arg Gln Gly Ser His Phe Met Pro Gly Ser Pro
    130                 135                 140
Leu Phe Arg Pro Gly Glu Lys Ala Ala Val Leu Thr Ser Thr Phe Ala
145                 150                 155                 160
Leu Ala Ala Phe Val Gly Phe Leu Gly Phe Leu Thr Trp Gln Phe Gly
            165                 170                 175
Trp Leu Phe Leu Leu Lys Phe Tyr Val Ala Pro Tyr Leu Val Phe Val
        180                 185                 190
Val Trp Leu Asp Leu Val Thr Phe Leu His His Thr Glu Asp Asn Ile
    195                 200                 205
Pro Trp Tyr Arg Gly Asp Asp Trp Tyr Phe Leu Lys Gly Ala Leu Ser
    210                 215                 220
Thr Ile Asp Arg Asp Tyr Gly Phe Ile Asn Pro Ile His His Asp Ile
225                 230                 235                 240
Gly Thr His Val Ala His His Ile Phe Ser Asn Met Pro His Tyr Lys
            245                 250                 255
Leu Arg Arg Ala Thr Glu Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr
        260                 265                 270
Arg Tyr Ser Asp Glu Pro Ile Trp Gln Ala Phe Phe Lys Ser Tyr Trp
    275                 280                 285
Ala Cys His Phe Val Pro Asn Gln Gly Ser Gly Val Tyr Tyr Gln Ser
    290                 295                 300
Pro Ser Asn Gly Gly Tyr Gln Lys Lys Pro Xaa Leu Ile Leu Ile Glu
305                 310                 315                 320
Ser Asn Gln His Arg Glu Gly Arg Gln Tyr Xaa Met Val Leu Leu Pro
            325                 330                 335
Ser Asp Arg Leu Met Arg Ser Met Glu Glu Val Lys Gln Ser His Ser
        340                 345                 350
Lys Arg Ser Ala Leu Asn Gln
        355

<210> 45
<211> 358
<212> PRT
<213> Saprolegnia diclina
```

```
<400> 45
Met Thr Glu Asp Lys Thr Lys Val Glu Phe Pro Thr Leu Thr Glu Leu
1               5                   10                  15
Lys His Ser Ile Pro Asn Ala Cys Phe Glu Ser Asn Leu Gly Leu Ser
            20                  25                  30
Leu Tyr Tyr Thr Ala Arg Ala Ile Phe Asn Ala Ser Ala Ser Ala Ala
        35                  40                  45
Leu Leu Tyr Ala Ala Arg Ser Thr Pro Phe Ile Ala Asp Asn Val Leu
    50                  55                  60
Leu His Ala Leu Val Cys Ala Thr Tyr Ile Tyr Val Gln Gly Val Ile
65                  70                  75                  80
Phe Trp Gly Phe Phe Thr Val Gly His Asp Cys Gly His Ser Ala Phe
                85                  90                  95
Ser Arg Tyr His Ser Val Asn Phe Ile Ile Gly Cys Ile Met His Ser
            100                 105                 110
Ala Ile Leu Thr Pro Phe Glu Ser Trp Arg Val Thr His Arg His His
        115                 120                 125
His Lys Asn Thr Gly Asn Ile Asp Lys Asp Glu Ile Phe Tyr Pro His
    130                 135                 140
Arg Ser Val Lys Asp Leu Gln Asp Val Arg Gln Trp Val Tyr Thr Leu
145                 150                 155                 160
Gly Gly Ala Trp Phe Val Tyr Leu Lys Val Gly Tyr Ala Pro Arg Thr
                165                 170                 175
Met Ser His Phe Asp Pro Trp Asp Pro Leu Leu Leu Arg Arg Ala Ser
            180                 185                 190
Ala Val Ile Val Ser Leu Gly Val Trp Ala Ala Phe Phe Ala Ala Tyr
        195                 200                 205
Ala Tyr Leu Thr Tyr Ser Leu Gly Phe Ala Val Met Gly Leu Tyr Tyr
    210                 215                 220
Tyr Ala Pro Leu Phe Val Phe Ala Ser Phe Leu Val Ile Thr Thr Phe
225                 230                 235                 240
Leu His His Asn Asp Glu Ala Thr Pro Trp Tyr Gly Asp Ser Glu Trp
                245                 250                 255
Thr Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala
            260                 265                 270
Phe Val Asp Asn Leu Ser His His Ile Gly Thr His Gln Val His His
        275                 280                 285
Leu Phe Pro Ile Ile Pro His Tyr Lys Leu Asn Glu Ala Thr Lys His
    290                 295                 300
Phe Ala Ala Ala Tyr Pro His Leu Val Arg Arg Asn Asp Glu Pro Ile
305                 310                 315                 320
Ile Thr Ala Phe Phe Lys Thr Ala His Leu Phe Val Asn Tyr Gly Ala
                325                 330                 335
Val Pro Glu Thr Ala Gln Ile Phe Thr Leu Lys Glu Ser Ala Ala Ala
            340                 345                 350
Ala Lys Ala Lys Ser Asp
            355


<210> 46
<211> 409
<212> PRT
<213> Caenorhabitis elegans

<220>
<221> VARIANT
<222> (389)...(389)
```

<223> Xaa = Unknown or Other at position 389

<400> 46
```
Val Thr Gly Gly Asp Val Leu Val Asp Ala Arg Ala Ser Leu Glu Glu
1               5                   10                  15
Lys Glu Ala Pro Arg Asp Val Asn Ala Asn Thr Lys Gln Ala Thr Thr
            20                  25                  30
Glu Glu Pro Arg Ile Gln Leu Pro Thr Val Asp Ala Phe Arg Arg Ala
        35                  40                  45
Ile Pro Ala His Cys Phe Glu Lys Arg Asp Leu Val Lys Ser Ile Arg Tyr
        50                  55                  60
Leu Val Gln Asp Phe Ala Ala Leu Thr Ile Leu Tyr Phe Ala Leu Pro
65                  70                  75                  80
Ala Phe Glu Tyr Phe Gly Leu Phe Gly Tyr Leu Val Trp Asn Ile Phe
                85                  90                  95
Met Gly Val Phe Gly Phe Ala Leu Phe Val Val Gly His Asp Cys Leu
            100                 105                 110
His Gly Ser Phe Ser Asp Asn Gln Asn Leu Asn Asp Phe Ile Gly His
        115                 120                 125
Ile Ala Phe Ser Pro Leu Phe Ser Pro Tyr Phe Pro Trp Gln Lys Ser
        130                 135                 140
His Lys Leu His His Ala Phe Thr Asn His Ile Asp Lys Asp His Gly
145                 150                 155                 160
His Val Trp Ile Gln Asp Lys Asp Trp Glu Ala Met Pro Ser Trp Lys
                165                 170                 175
Arg Trp Phe Asn Pro Ile Pro Phe Ser Gly Trp Leu Lys Trp Phe Pro
            180                 185                 190
Val Tyr Thr Leu Phe Gly Phe Cys Asp Gly Ser His Phe Trp Pro Tyr
        195                 200                 205
Ser Ser Leu Phe Val Arg Asn Ser Asp Arg Val Gln Cys Val Ile Ser
210                 215                 220
Gly Ile Cys Cys Cys Val Cys Ala Tyr Ile Ala Leu Thr Ile Ala Gly
225                 230                 235                 240
Ser Tyr Ser Asn Trp Phe Trp Tyr Tyr Trp Val Pro Leu Ser Phe Phe
            245                 250                 255
Gly Leu Met Leu Val Ile Val Thr Tyr Leu Gln His Val Asp Asp Val
        260                 265                 270
Ala Glu Val Tyr Glu Ala Asp Glu Trp Ser Phe Val Arg Gly Gln Thr
    275                 280                 285
Gln Thr Ile Asp Arg Tyr Tyr Gly Leu Gly Leu Asp Thr Thr Met His
    290                 295                 300
His Ile Thr Asp Gly His Val Ala His His Phe Phe Asn Lys Ile Pro
305                 310                 315                 320
His Tyr His Leu Ile Glu Ala Thr Glu Gly Val Lys Lys Val Leu Glu
            325                 330                 335
Pro Leu Ser Asp Thr Gln Tyr Gly Tyr Lys Ser Gln Val Asn Tyr Asp
        340                 345                 350
Phe Phe Ala Arg Phe Leu Trp Phe Asn Tyr Lys Leu Asp Tyr Leu Val
        355                 360                 365
His Lys Thr Ala Gly Ile Met Gln Phe Arg Thr Thr Leu Glu Glu Lys
370                 375                 380
Ala Lys Ala Lys Xaa Lys Asn Ile Pro Cys Arg Ser Arg Val Gln Gln
385                 390                 395                 400
Gln Leu Leu Arg Phe His Arg Phe Cys
                405
```

<210> 47

<211> 333
<212> PRT
<213> Saprolegnia diclina

<400> 47
Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala
1   5   10   15
Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Leu Glu Pro
            20   25   30
Pro Thr Ile Thr Leu Lys Asp Leu Arg Ala Ala Ile Pro Ala His Cys
        35   40   45
Phe Glu Arg Ser Ala Ala Thr Ser Phe Tyr His Leu Ala Lys Asn Leu
    50   55   60
Ala Ile Cys Ala Gly Val Phe Ala Val Gly Leu Lys Leu Ala Ala Ala
65   70   75   80
Asp Leu Pro Leu Ala Ala Lys Leu Val Ala Trp Pro Ile Tyr Trp Phe
                85   90   95
Val Gln Gly Thr Tyr Phe Thr Gly Ile Trp Val Ile Ala His Glu Cys
            100   105   110
Gly His Gln Ala Phe Ser Ala Ser Glu Ile Leu Asn Asp Thr Val Gly
        115   120   125
Ile Ile Leu His Ser Leu Leu Phe Val Pro Tyr His Ser Trp Lys Ile
    130   135   140
Thr His Arg Arg His His Ser Asn Thr Gly Ser Cys Glu Asn Asp Glu
145   150   155   160
Val Phe Thr Pro Thr Pro Arg Ser Val Val Glu Ala Lys His Asp His
                165   170   175
Ser Leu Leu Glu Glu Ser Pro Leu Tyr Asn Leu Tyr Gly Ile Val Met
            180   185   190
Met Leu Leu Val Gly Trp Met Pro Gly Tyr Leu Phe Phe Asn Ala Thr
        195   200   205
Gly Pro Gly Thr Lys Tyr Ala Gly Leu Ala Lys Ser His Phe Asn Pro Tyr
    210   215   220
Ala Ala Phe Phe Leu Pro Lys Glu Arg Leu Ser Ile Trp Trp Ser Asp
225   230   235   240
Leu Cys Phe Leu Ala Ala Leu Tyr Gly Phe Gly Tyr Gly Val Ser Val
                245   250   255
Phe Gly Leu Leu Asp Val Ala Arg His Tyr Ile Val Pro Tyr Leu Ile
            260   265   270
Cys Asn Ala Tyr Leu Val Leu Ile Thr Tyr Leu Gln His Thr Asp Thr
        275   280   285
Thr Pro Leu Leu Gly Lys Tyr Tyr Leu Ile Asp Pro Thr Pro Ile Pro
    290   295   300
Leu Ala Leu Trp Arg Ser Phe Thr His Cys Lys Tyr Val Glu Asp Asp
305   310   315   320
Gly Asn Val Val Phe Tyr Lys Arg Lys Leu Glu Glu Lys
                325   330

<210> 48
<211> 412
<212> PRT
<213> Gossypium hirsutum

<220>
<221> VARIANT
<222> (9)...(9)
<223> Xaa = Unknown or Other at position 9

<221> VARIANT
<222> (403)...(403)
<223> Xaa = Unknown or Other at position 403

<400> 48

```
Leu Arg Val Ser Ser Thr Trp Arg Xaa Thr Ala Phe Phe Lys Ala Ser
1               5                   10                  15
Lys Met Gly Ala Gly Gly Arg Met Pro Ile Asp Gly Ile Lys Glu Glu
        20                  25                  30
Asn Arg Gly Ser Val Asn Arg Val Pro Ile Glu Lys Pro Pro Phe Thr
        35                  40                  45
Leu Gly Gln Ile Lys Gln Ala Ile Pro Pro His Cys Phe Arg Arg Ser
50                  55                  60
Leu Leu Arg Ser Phe Ser Tyr Val Val His Asp Leu Cys Leu Ala Ser
65              70                  75                  80
Phe Phe Tyr Tyr Ile Ala Thr Ser Tyr Phe His Phe Leu Pro Gln Pro
                85                  90                  95
Phe Ser Tyr Ile Ala Trp Pro Val Tyr Trp Val Leu Gln Gly Cys Ile
            100                 105                 110
Leu Thr Gly Val Trp Val Ile Ala His Glu Trp Gly His His Ala Phe
        115                 120                 125
Arg Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Leu Ile Leu His Ser
        130                 135                 140
Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Ile Ser His Arg Arg His
145                 150                 155                 160
His Ser Asn Thr Gly Ser Met Glu Arg Asp Glu Val Phe Val Pro Lys
                165                 170                 175
Pro Lys Ser Lys Leu Ser Cys Phe Ala Lys Tyr Leu Asn Asn Pro Pro
            180                 185                 190
Gly Arg Val Leu Ser Leu Val Val Thr Leu Thr Leu Gly Trp Pro Met
        195                 200                 205
Tyr Leu Ala Phe Asn Val Ser Gly Arg Tyr Tyr Asp Arg Leu Ala Ser
210                 215                 220
His Tyr Asn Pro Tyr Gly Pro Ile Tyr Ser Asp Arg Glu Arg Leu Gln
225                 230                 235                 240
Val Tyr Ile Ser Asp Thr Gly Ile Phe Ala Val Ile Tyr Val Leu Tyr
            245                 250                 255
Lys Ile Ala Ala Thr Lys Gly Leu Ala Trp Leu Leu Cys Thr Tyr Gly
        260                 265                 270
Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
        275                 280                 285
Gln His Thr His Ser Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
        290                 295                 300
Trp Leu Arg Gly Ala Leu Ser Thr Met Asp Arg Asp Phe Gly Val Leu
305                 310                 315                 320
Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
            325                 330                 335
Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
            340                 345                 350
Lys Pro Ile Leu Gly Lys Tyr Tyr Pro Phe Asp Gly Thr Pro Ile Tyr
        355                 360                 365
Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro Asp
        370                 375                 380
Val Gly Gly Gly Gly Gly Ser Lys Gly Val Phe Trp Tyr Arg Asn
385                 390                 395                 400
Lys Phe Xaa Arg Pro Thr Asn Cys Leu Ile Ala Gly
```

                    405   410

```
<210> 49
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 1 from Example 3

<400> 49
Thr Arg Ala Ala Ile Pro Lys His Cys Trp Val Lys
 1               5                   10


<210> 50
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 2 from Example 3

<400> 50
Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser
 1               5                   10                  15


<210> 51
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 3 from Example 3

<400> 51
Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn
 1               5                   10                  15


<210> 52
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 4 from Example 3

<221> VARIANT
<222> (5)...(5)
<223> Xaa = D or H at position 5

<221> VARIANT
<222> (7)...(7)
<223> Xaa = D or Y at position 7

<400> 52
Gly Ser His Phe Xaa Pro Xaa Ser Asp Leu Phe Val
 1               5                   10
```

```
<210> 53
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 5 from Example 3

<221> VARIANT
<222> (3)...(3)
<223> Xaa = Y or F at position 3

<221> VARIANT
<222> (4)...(4)
<223> Xaa = L or V at position 4

<221> VARIANT
<222> (11)...(11)
<223> Xaa = L or I at position 11

<400> 53
Trp Ser Xaa Xaa Arg Gly Gly Leu Thr Thr Xaa Asp Arg
 1               5                   10


<210> 54
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 6 from Example 3

<400> 54
His His Asp Ile Gly Thr His Val Ile His His Leu Phe Pro Gln
 1               5                   10                  15

<210> 55
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 7 from Example 3

<221> VARIANT
<222> (2)...(2)
<223> Xaa = L or F at position 2

<221> VARIANT
<222> (5)...(5)
<223> Xaa = Q or K at position 5

<221> VARIANT
<222> (12)...(12)
<223> Xaa = V or I at position 12
```

<400> 55
His Xaa Phe Pro Xaa Ile Pro His Tyr His Leu Xaa Glu Ala Thr
1   5   10   15

<210> 56
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 8 from Example 3

<221> VARIANT
<222> (3)...(3)
<223> Xaa = A or I at position 3

<221> VARIANT
<222> (6)...(6)
<223> Xaa = L or F at position 6

<400> 56
His Val Xaa His His Xaa Phe Pro Gln Ile Pro His Tyr His Leu
1   5   10   15

<210> 57
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 1 from Example 7

<221> VARIANT
<222> (2)...(2)
<223> Xaa = N or E at position 2

<221> VARIANT
<222> (10)...(10)
<223> Xaa = D or E at position 10

<221> VARIANT
<222> (11)...(11)
<223> Xaa = A or C at position 11

<400> 57
Pro Xaa Phe Thr Ile Lys Glu Ile Arg Xaa Xaa Ile Pro Ala His Cys
1   5   10   15
Phe

<210> 58
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 2 from Example 7

```
<221> VARIANT
<222> (3)...(3)
<223> Xaa = H or F at position 3

<221> VARIANT
<222> (11)...(11)
<223> Xaa = V or Y at position 11

<221> VARIANT
<222> (13)...(13)
<223> Xaa = I or L at position 13

<221> VARIANT
<222> (16)...(16)
<223> Xaa = A or L at position 16

<400> 58
Met Pro Xaa Tyr His Ala Glu Glu Ala Thr Xaa His Xaa Lys Lys Xaa
 1               5                  10                  15

<210> 59
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 3 from Example 7

<221> VARIANT
<222> (2)...(2)
<223> Xaa = L or V at position 2

<221> VARIANT
<222> (5)...(5)
<223> Xaa = A or I at position 5

<221> VARIANT
<222> (6)...(6)
<223> Xaa = C or M or A at position 6

<221> VARIANT
<222> (9)...(9)
<223> Xaa = V or I at position 9

<221> VARIANT
<222> (11)...(11)
<223> Xaa = L or G or C at position 11

<400> 59
Pro Xaa Tyr Trp Xaa Xaa Gln Gly Xaa Val Xaa Thr Gly Val Trp
 1               5                  10                  15

<210> 60
<211> 15
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Protein Motif 4 from Example 7

<221> VARIANT
<222> (6)...(6)
<223> Xaa = L or F at position 6

<221> VARIANT
<222> (9)...(9)
<223> Xaa = T or Q at position 9

<400> 60
His Val Ala His His Xaa Phe Ser Xaa Met Pro His Tyr His Ala
 1               5                  10                  15
```